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# GNPAnnot Community Annotation System Applied To Sugarcane BAC Clone Sequences

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A large amount of data is being produced by current genome sequencing projects. Sequence annotations and analyses need to be organized into databases and widely accessible. Like other species, sugarcane would benefit from centralized and innovative systems to study its genome. The GNPAnnot community annotation system (CAS) could be particularly relevant to the SUGESI sequencing project. It consists in a system for structural and functional annotations supported by comparative genomics allowing both automatic predictions and manual curations of genes and transposable elements. The core of the GNPAnnot CAS dedicated to tropical plants is made of GMOD components.The Chado database can be browsed using the Generic Genome Browser (GBrowse) which provides links to genome editors (ie. Artemis and Apollo). We developed the Chado controller in order to manage public and private annotation projects. It also provides an annotation history page for each gene or transposable element and an annotation inspector that automates several tasks and reports annotation mistakes. GNPAnnot CAS has already been used to annotate sugarcane BAC clones sequences and could be useful to facilitate the annotation of novel sugarcane sequences.

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